

09045001001

5' NNC TCC CGC AGC CGC AGC CGC CGT GCT CAG CGC GAG CCC CGG AGC CCT TGA GCG

CGA GGC GCG GAG CCC CGG AGC CCC CAA ACC GCA GAC ACA TCC CCG CGC CCC AGA

GCC CCG GCC TGC GCG CCC AGC CGG GCC CGC GCG ATG CCC TCA GAC CGG CCT TTC

M P S D R P F

AAG CAG CGG CGG AGC TTC GCC GAC CGC TGT AAG GAG GTA CAG CAG ATC CGC GAC

K Q R R S F A D R C K E V Q Q I R D

CAG CAC CCC AGC AAA ATC CCG GTG ATC ATC GAG CGC TAC AAG GGT GAG AAG CAG

Q H P S K I P V I I E R Y K G E K Q

CTG CCC GTC CTG GAC AAG ACC AAG TTT TTG GTC CCG GAC CAT GTC AAC ATG AGC

L P V L D K T K F L V P D H V N M S

GAG TTG GTC AAG ATC ATC CGG CGC CGC CTG CAG CTG AAC CCC ACG CAG GCC TTC

E L V K I I R R R L Q L N P T Q A F

TTC CTG CTG GTG AAC CAG CAC AGC ATG GTG AGT GTG TCC ACG CCC ATC GCG GAC

F L L V N Q H S M V S V S T P I A D

ATC TAC GAG CAG GAG AAA GAC GAG GAC GGC TTC CTC TAT ATG GTC TAC GCC TCC

I Y E Q E K D E D G F L Y M V Y A S

CAG GAA ACC TTC GGC TTC TGA GCC AGC AGT AGG GGG GCT CGG CCT GGG AGT CGG

Q E T F G F

GGG GCC CCG GTC AGG CCC TGC CCA GAG AGC TTC TGG TTC CTG AAC TGA GCT GCC

TCT ACC GTG GTG GGC TGG GCA GGC ATG TGC CCC CCT AGT CAG AGG GCA 3'

FIGURE 1

| | | |
|-----|--|-----------|
| 1 | MPSDRPFKQRRSFADRCKEVQQIRDQHP | 1441378 |
| 1 | MPSDKTKQRRSEQRVEDVRLIREQHPTKIPVIERYKG | GI 455109 |
| 41 | EKQLPVLDKTKFLVPPDHVNMSELVKIIRRRLQLNPTQAF | 1441378 |
| 41 | EKQLPVLDKTKFLVPPDHVNMSELVKIIRRRLQLNPTQAF | GI 455109 |
| 81 | LLVNQHSMVSVSTPIADIYEQEKDEDEGFLYMVVYASQETFG | 1441378 |
| 81 | LLVNGHSMVSVSTPISEVYESERDEDEGFLYMVVYASQETFG | GI 455109 |
| 121 | -----F----- | |
| 121 | TALAVTYMSALKATATGREPCL | 1441378 |
| | | GI 455109 |

FIGURE 2

102120-60940660

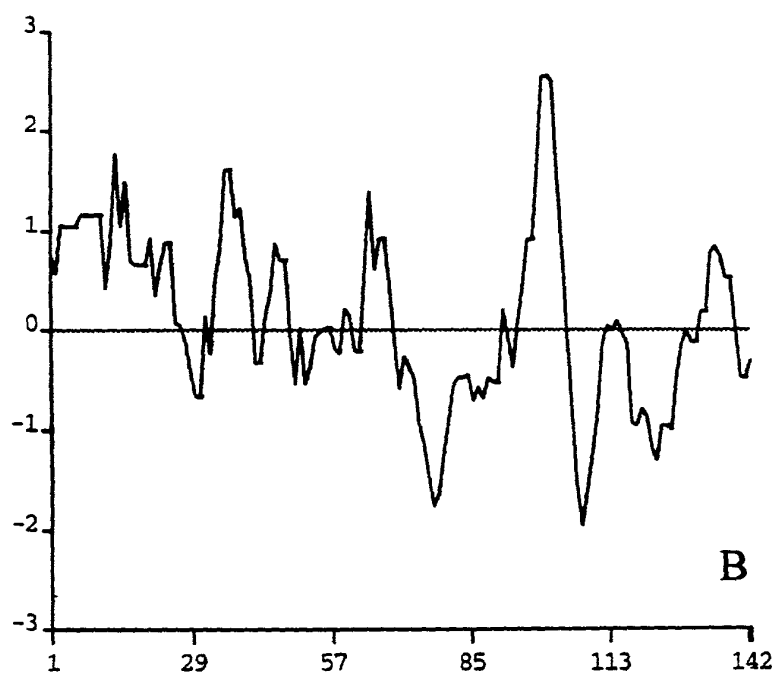
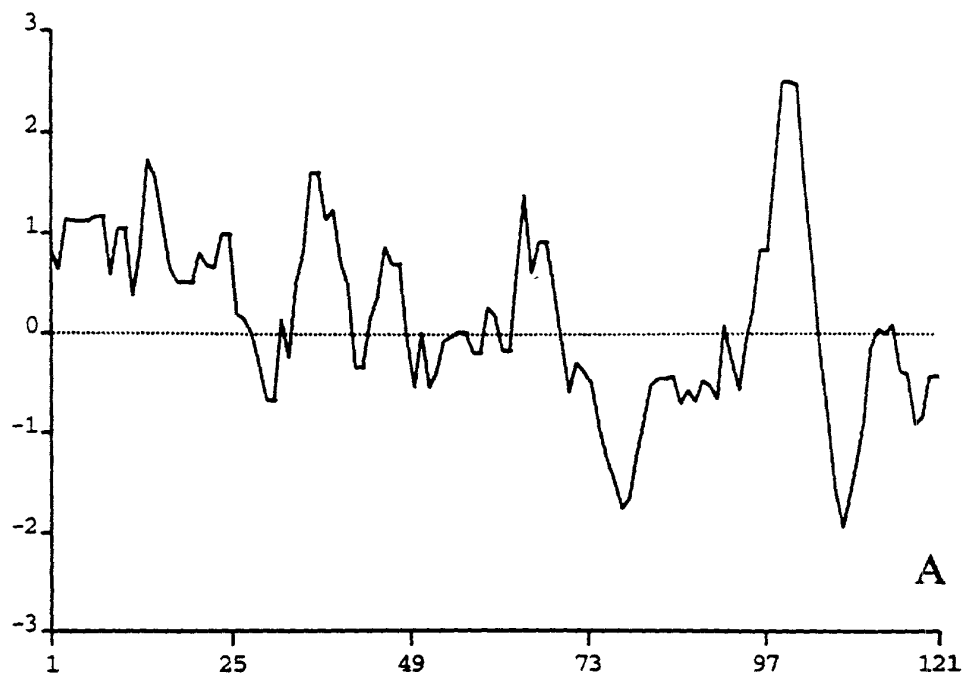


FIGURE 3